In the Specification:

Please replace the paragraph beginning on page 2, line 29, and continuing on to page 3, with the following:

The testes cDNA library was screened using pooled allogeneic prostate cancer patients' sera. Seven reactive clones were purified, *in vivo* excised, and converted to plasmid forms. cDNA inserts were analysed using restriction mapping and cDNA sequencing. Comparison to the ~~Genbank~~ Genbank® non-redundant and expressed sequence tag (EST) databases revealed that these 7 clones represented 6 distinct genes, 5 previously unknown genes and 1 known gene. T128 was fully sequenced and is described here; the following results are consistent with T128 being a cancer-testis (CT) associated gene, the predicted protein of which it is believed will act as a new target antigen for immunotherapy.

Please replace the paragraph beginning on page 3, line 4 with the following:

T128 overlaps with a predicted, hypothetical coding sequence submitted to ~~Genbank~~ Genbank® as accession number FLJ10330. The function and isolation of this was not referred to. This hypothetical sequence was apparently found by Lee S.Y., *et al.* (PNAS, (2003), Vol. 100(5), pages 2651-2656) to be similar to an antigen found by serological analysis of cDNA expression libraries (clone NY-SAR-27). However, information published on this clone is limited and only seems to refer to a partial CDS. T128 is the full CDS. Furthermore, NY-SAR-27 is only mentioned in passing by Lee and was not developed further, presumably due to the limited reactivity observed (only 2 out of 39 sarcoma sera). This is in contrast with the full sequence now identified by the inventors and unexpectedly found to have considerably greater potential.

Please replace the paragraph on page 17, line 35, continuing on to page 18, with the following:

The ~~Mx4000~~ Mx4000® apparatus measures the fluorescence of each sample at the end of the annealing step, and at the end of each cycle when creating the dissociation curve.

After the RT-PCR reaction, the software program plots linear values of fluorescence (dRn) against cycle number. After background adjustment, the Ct value, which is defined as the number of cycles at which the reaction crosses a threshold value, i.e. the fluorescence due to the RT-PCR product exceeds the background level, is calculated for each sample by the software. The software produces a standard curve by measuring the Ct value of each standard and plotting it against the approximate concentrations for the corresponding standard dilution. The expression level of the unknown genes in a given RNA sample are then normalised to the housekeeping gene GAPDH. The normalised expression of each gene is calculated by dividing the Ct value for the unknown gene in a sample by the Ct value for GAPDH in the same sample. Thus, a sample with high level expression of a gene will have a lower Ct value because the gene is more abundant, hence it takes less cycles for the fluorescence to exceed that of background levels. Therefore, when calculating the normalised expression for that gene the Ct value would be lower than a gene that is less abundant. This should be remembered when observing the normalised expression graphs because the lower the Ct value the more abundant the gene is in the sample. Derivation of this fraction is independent of RNA sample concentration, eliminating the requirement to measure RNA concentration accurately.

Please replace the paragraph on page 18, line 18 with the following:

The RT-Q-PCR reactions were performed in the ~~Mx4000~~ Mx4000® QPCR system (Stratagene, UK) using SYBR green fluorescent dye (Yin, J.L. *et al.*, 2001. Immuno. Cell Biol. 79(3):213-21). RNA samples were DNase treated in order to remove genomic DNA following standard protocols. Thermocycling for each reaction was done in a final volume of 25 µl containing 1 µl of template (1:10 diluted), or standard, 12.5 µl SYBR green master mix (Qiagen, UK) containing Hot Start®Taq DNA polymerase, reaction buffer, ROX reference dye, SYBR green dye, magnesium chloride and deoxynucleotides, and pre-optimised amounts of gene-specific forward and reverse primers. This was then made up to 25 µl with Qiagen water. In each experiment a minimum of 8 no-template controls should be included to ensure no contamination has occurred and also to indicate the degree of amplification due to primer dimers. Also included were 4 RT-negative (no reverse transcription) samples to ensure that genomic DNA had been completely removed following DNase treatment.

Please replace the paragraph beginning on page 18, line 35 and continuing to page 19, lines 1-2, with the following:

In *silico* analysis of T128

The amino acid sequence of T128 was analysed using search programs including PROSITE ~~(accessible at www.expasy.ch/prosite/)~~, PSORT ~~(accessible at http://psort.nibb.ac.jp)~~ and Pfam ~~(accessible at http://www.sanger.ac.uk/cgi-bin/Pfam/nph-search.cgi)~~. These identified:

Please replace the paragraph beginning on page 20, line 28, with the following:

T128 was sequenced and the homology of sequence was compared with homologous sequences on ~~Genbank~~ Genbank®. This showed some overlap with a hypothetical protein, FLJ10330.